

RAW SEQUENCE LISTING

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Application Serial Number: 10/550,768
Source: PCT
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PATENT APPLICATION: US/10/550,768

DATE: 10/07/2005
TIME: 09:30:19

Input Set : A:\298641 sequence listing.txt
Output Set: N:\CRF4\10072005\J550768.raw

4 <110> APPLICANT: Meritet, Jean-Francois
5 Dron, Michel
6 Tovey, Michael Gerard
9 <120> TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
11 <130> FILE REFERENCE: 046658/298641
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/550,768
C--> 13 <141> CURRENT FILING DATE: 2005-09-27
13 <160> NUMBER OF SEQ ID NOS: 2
15 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 6045
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (243)..(5381)
27 <223> OTHER INFORMATION:
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31 agcgggctgg gtcctaggcc aggtctgggg taacctggaa cttccacctg ggctctgcgc 60
32 taggtctctg tttcaactccc tccccgcggg gcgcgcagct cgcgggtctt tggacaccac 120
33 cggtcctgag tccgcggact gccatttca ttaagaactg ccacttagag gtacccaaat 180
34 aaagggtatt tgctacccctt aatacttgcc agttcaggtt ggaggcacag gcagcagcaa 240
36 ga atg gaa aga aat gtt ctt aca aca ttt tca cag gaa atg tcc cag 287
37 Met Glu Arg Asn Val Leu Thr Thr Phe Ser Gln Glu Met Ser Gln
38 1 5 10 15
40 tta att ttg aat gaa atg cca aaa gct gaa tat tcc agt tta ttc aat 335
41 Leu Ile Leu Asn Glu Met Pro Lys Ala Glu Tyr Ser Ser Leu Phe Asn
42 20 25 30
44 gat ttt gtt gaa tct gaa ttt ttt ttg att gat ggg gat tca tta ctt 383
45 Asp Phe Val Glu Ser Glu Phe Phe Leu Ile Asp Gly Asp Ser Leu Leu
46 35 40 45
48 atc aca tgt atc tgt gag ata tca ttt aag cct ggg cag aac ctc cat 431
49 Ile Thr Cys Ile Cys Glu Ile Ser Phe Lys Pro Gly Gln Asn Leu His
50 50 55 60
52 ttc ttc tat ctg gtt gaa cgc tat ctt gtg gat ctt att agc aaa gga 479
53 Phe Phe Tyr Leu Val Glu Arg Tyr Leu Val Asp Leu Ile Ser Lys Gly
54 65 70 75
56 gga caa ttc acc ata gtt ttc ttc aag gat gcc gag tat gcg tat ttc 527
57 Gly Gln Phe Thr Ile Val Phe Phe Lys Asp Ala Glu Tyr Ala Tyr Phe
58 80 85 90 95
59 aac ttc cct gaa ctt ctt tct ttg aga act gct tta att ctt cat ctt 575
60 Asn Phe Pro Glu Leu Leu Ser Leu Arg Thr Ala Leu Ile Leu His Leu
61 100 105 110

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63 cag aag aat acc acc att gat gtt cga aca aca ttt tcg aga tgc tta	623
64 Gln Lys Asn Thr Thr Ile Asp Val Arg Thr Thr Phe Ser Arg Cys Leu	
65 115 120 125	
67 tca aaa gag tgg gga agt ttc ttg gaa gag agt tac cca tat ttc ctg	671
68 Ser Lys Glu Trp Gly Ser Phe Leu Glu Ser Tyr Pro Tyr Phe Leu	
69 130 135 140	
71 ata gtt gca gac gaa ggc ctg aac gat cta caa aca cag ctt ttc aac	719
72 Ile Val Ala Asp Glu Gly Leu Asn Asp Leu Gln Thr Gln Leu Phe Asn	
73 145 150 155	
75 ttt tta atc att cat tct tgg gca agg aag gtc aac gtt gta ctt tcc	767
76 Phe Leu Ile Ile His Ser Trp Ala Arg Lys Val Asn Val Val Leu Ser	
77 160 165 170 175	
79 tca ggg caa gaa tct gat gtt ctt tgc ctt tat gca tac ctt ctt cca	815
80 Ser Gly Gln Glu Ser Asp Val Leu Cys Leu Tyr Ala Tyr Leu Leu Pro	
81 180 185 190	
83 agc atg tac aga cac cag att ttt tcc tgg aag aat aag cag aac att	863
84 Ser Met Tyr Arg His Gln Ile Phe Ser Trp Lys Asn Lys Gln Asn Ile	
85 195 200 205	
87 aaa gat gct tat aca acc ctg ctt aac cag ttg gaa aga ttt aag ctt	911
88 Lys Asp Ala Tyr Thr Leu Leu Asn Gln Leu Glu Arg Phe Lys Leu	
89 210 215 220	
91 tca gca tta gca cct ctt ttt gga agt tta aaa tgg aat aat att acg	959
92 Ser Ala Leu Ala Pro Leu Phe Gly Ser Leu Lys Trp Asn Asn Ile Thr	
93 225 230 235	
95 gaa gag gca cac aag act gta tct ctg ctt aca caa gtc tgg cca gaa	1007
96 Glu Glu Ala His Lys Thr Val Ser Leu Leu Thr Gln Val Trp Pro Glu	
97 240 245 250 255	
99 gga tct gac att cgg cgt gtc ttt tgt gtt act tca tgc tca tta tct	1055
100 Gly Ser Asp Ile Arg Arg Val Phe Cys Val Thr Ser Cys Ser Leu Ser	
101 260 265 270	
103 ttg aga atg tac cat cgc ttt tta gga aac aga gag ccc tcc tct ggt	1103
104 Leu Arg Met Tyr His Arg Phe Leu Gly Asn Arg Glu Pro Ser Ser Gly	
105 275 280 285	
107 cag gaa act gag atc caa cag gtg aac agt aat tgc tta acc ctg cag	1151
108 Gln Glu Thr Glu Ile Gln Gln Val Asn Ser Asn Cys Leu Thr Leu Gln	
109 290 295 300	
110 gag atg gaa gat ttg tgt aaa ctg cat tgt ctc act gtg gtt ttt cta	1199
111 Glu Met Glu Asp Leu Cys Lys Leu His Cys Leu Thr Val Val Phe Leu	
112 305 310 315	
114 ctc cat ctg cct ctt tct caa aga gct tgt gct aga gtc atc act tcc	1247
115 Leu His Leu Pro Leu Ser Gln Arg Ala Cys Ala Arg Val Ile Thr Ser	
116 320 325 330 335	
118 cat tgg gct gag gac atg aag cct tta tta caa atg aaa aag tgg tgt	1295
119 His Trp Ala Glu Asp Met Lys Pro Leu Leu Gln Met Lys Lys Trp Cys	
120 340 345 350	
122 gaa tat ttc atc tta aga aat ata cat act ttt gaa ttt tgg aat ctg	1343
123 Glu Tyr Phe Ile Leu Arg Asn Ile His Thr Phe Glu Phe Trp Asn Leu	
124 355 360 365	
126 aat tta att cac ctt tct gac tta aat gat gag ctt ttg tgg aag aat	1391

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127 Asn Leu Ile His Leu Ser Asp Leu Asn Asp Glu Leu Leu Leu Lys Asn		
128 370 375 380		
130 att gct ttt tac tat gaa aat gaa aat gta aaa ggc cta cat ttg aat	1439	
131 Ile Ala Phe Tyr Tyr Glu Asn Glu Asn Val Lys Gly Leu His Leu Asn		
132 385 390 395		
134 ttg gga gat acc att atg aaa gat tat gaa tat ctc tgg aat acc gta	1487	
135 Leu Gly Asp Thr Ile Met Lys Asp Tyr Glu Tyr Leu Trp Asn Thr Val		
136 400 405 410 415		
138 tca aag ttg gtc aga gac ttt gag gtt gga cag cca ttt cct ctg aga	1535	
139 Ser Lys Leu Val Arg Asp Phe Glu Val Gly Gln Pro Phe Pro Leu Arg		
140 420 425 430		
142 aca aca aaa gtt tgt ttt ctt gga aag aaa cca tca cca atc aaa gac	1583	
143 Thr Thr Lys Val Cys Phe Leu Gly Lys Lys Pro Ser Pro Ile Lys Asp		
144 435 440 445		
146 agc tcc aat gaa atg gtg ccc aat ttg ggt ttt att cca acg tca tct	1631	
147 Ser Ser Asn Glu Met Val Pro Asn Leu Gly Phe Ile Pro Thr Ser Ser		
148 450 455 460		
150 ttt gtg gtt gat aaa ttt gct gga gat att ttg aaa gat ttg cct ttt	1679	
151 Phe Val Val Asp Lys Phe Ala Gly Asp Ile Leu Lys Asp Leu Pro Phe		
152 465 470 475		
154 cta aag agt gat gat cct att gtt act tca ctg gtt aaa caa aag gaa	1727	
155 Leu Lys Ser Asp Asp Pro Ile Val Thr Ser Leu Val Lys Gln Lys Glu		
156 480 485 490 495		
158 ttt gat gaa ctt gtg cac tgg cat tct cat aaa ccc ctg agt gat gat	1775	
159 Phe Asp Glu Leu Val His Trp His Ser His Lys Pro Leu Ser Asp Asp		
160 500 505 510		
161 tat gac agg tcc agg tgt cag ttt gat gaa aaa tct aga gac cct cgt	1823	
162 Tyr Asp Arg Ser Arg Cys Gln Phe Asp Glu Lys Ser Arg Asp Pro Arg		
163 515 520 525		
165 gtt ctt aga tct gtg caa aag tat cat gtt ttc caa cgg ttt tat ggg	1871	
166 Val Leu Arg Ser Val Gln Lys Tyr His Val Phe Gln Arg Phe Tyr Gly		
167 530 535 540		
169 aat tca tta gaa aca gtc tct tcg aaa atc atc gtg act caa act att	1919	
170 Asn Ser Leu Glu Thr Val Ser Ser Lys Ile Ile Val Thr Gln Thr Ile		
171 545 550 555		
173 aag tca aag aag gat ttt agt ggg ccc aag agc aaa aag gca cac gag	1967	
174 Lys Ser Lys Lys Asp Phe Ser Gly Pro Lys Ser Lys Lys Ala His Glu		
175 560 565 570 575		
177 acc aag gct gaa ata att gct aga gag aat aag aaa agg tta ttt gcc	2015	
178 Thr Lys Ala Glu Ile Ile Ala Arg Glu Asn Lys Lys Arg Leu Phe Ala		
179 580 585 590		
181 agg gaa gaa caa aag gaa gag caa aag tgg aat gct ttg tca ttt tct	2063	
182 Arg Glu Glu Gln Lys Glu Glu Gln Lys Trp Asn Ala Leu Ser Phe Ser		
183 595 600 605		
185 att gaa gag caa ttg aaa gaa aat tta cac tct gga ata aag agc ctg	2111	
186 Ile Glu Glu Gln Leu Lys Glu Asn Leu His Ser Gly Ile Lys Ser Leu		
187 610 615 620		
189 gaa gat ttt ttg aaa tcc tgt aaa agt agc tgt gtg aaa ctt cag gtt	2159	
190 Glu Asp Phe Leu Lys Ser Cys Lys Ser Ser Cys Val Lys Leu Gln Val		

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191	625	630	635	
193	gaa atg gtg ggg tta act gct tgc ttg aaa gcc tgg aaa gaa cat tgc			2207
194	Glu Met Val Gly Leu Thr Ala Cys Leu Lys Ala Trp Lys Glu His Cys			
195	640	645	650	655
197	cga agt gaa gaa ggt aaa acc acg aaa gat tta agt ata gct gtt cag			2255
198	Arg Ser Glu Glu Gly Lys Thr Thr Lys Asp Leu Ser Ile Ala Val Gln			
199	660	665	670	
201	gtg atg aaa agg atc cac tcc ttg atg gaa aaa tac tca gaa ctt tta			2303
202	Val Met Lys Arg Ile His Ser Leu Met Glu Lys Tyr Ser Glu Leu Leu			
203	675	680	685	
205	caa gaa gat gat cgg caa ctc ata gcc aga tgc ctt aag tat tta gga			2351
206	Gln Glu Asp Asp Arg Gln Leu Ile Ala Arg Cys Leu Lys Tyr Leu Gly			
207	690	695	700	
209	ttt gat gag ttg gca agt tct tta cat cca gcc cag gat gca gaa aat			2399
210	Phe Asp Glu Leu Ala Ser Ser Leu His Pro Ala Gln Asp Ala Glu Asn			
211	705	710	715	
212	gat gta aaa gtg aag aaa agg aat aaa tat tca att ggc att ggg cca			2447
213	Asp Val Lys Val Lys Lys Arg Asn Lys Tyr Ser Ile Gly Ile Gly Pro			
214	720	725	730	735
216	gct cgg ttc caa ctg caa tac atg ggc cat tat ttg ata cga gat gag			2495
217	Ala Arg Phe Gln Leu Gln Tyr Met Gly His Tyr Leu Ile Arg Asp Glu			
218	740	745	750	
220	aga aaa gac cca gat ccc agg gtc cag gat ttt att ccc gac aca tgg			2543
221	Arg Lys Asp Pro Asp Pro Arg Val Gln Asp Phe Ile Pro Asp Thr Trp			
222	755	760	765	
224	cag cga gag ctc ctt gat gtt gtg gat aag aat gag tca gca gtg att			2591
225	Gln Arg Glu Leu Leu Asp Val Val Asp Lys Asn Glu Ser Ala Val Ile			
226	770	775	780	
228	gtt gcc cca acg tcc tca ggc aaa aca tat gcc tcc tac tac tgt atg			2639
229	Val Ala Pro Thr Ser Ser Gly Lys Thr Tyr Ala Ser Tyr Tyr Cys Met			
230	785	790	795	
232	gag aaa gtg ctg aag gag agc gac gac ggg gtg gtc gtg tac gtt gca			2687
233	Glu Lys Val Leu Lys Glu Ser Asp Asp Gly Val Val Val Tyr Val Ala			
234	800	805	810	815
236	ccc aca aag gcc ctt gtt aat caa gtg gca gca act gtt cag aat cgt			2735
237	Pro Thr Lys Ala Leu Val Asn Gln Val Ala Ala Thr Val Gln Asn Arg			
238	820	825	830	
240	ttt acg aaa aat ctg cca agt ggt gaa gtt ctc tgt ggt gtt ttc acc			2783
241	Phe Thr Lys Asn Leu Pro Ser Gly Glu Val Leu Cys Gly Val Phe Thr			
242	835	840	845	
244	agg gag tat cgt cat gat gcc tta aac tgt cag gta ctt att aca gtg			2831
245	Arg Glu Tyr Arg His Asp Ala Leu Asn Cys Gln Val Leu Ile Thr Val			
246	850	855	860	
248	cct gcc tgc ttt gaa att ctg ctg ctt gct cct cat cgc caa aac tgg			2879
249	Pro Ala Cys Phe Glu Ile Leu Leu Ala Pro His Arg Gln Asn Trp			
250	865	870	875	
252	gtg aaa aag atc aga tat gtt ata ttt gat gag gtt cat tgt ctt ggt			2927
253	Val Lys Lys Ile Arg Tyr Val Ile Phe Asp Glu Val His Cys Leu Gly			
254	880	885	890	895

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256 gga gaa att gga gca gaa atc tgg gaa cat ctc ctt gtc atg atc cga	2975
257 Gly Glu Ile Gly Ala Glu Ile Trp Glu His Leu Leu Val Met Ile Arg	
258 900 905 910	
260 tgt ccc ttt ttg gct ctt tca gct acc ata agt aat cct gaa cat ctc	3023
261 Cys Pro Phe Leu Ala Leu Ser Ala Thr Ile Ser Asn Pro Glu His Leu	
262 915 920 925	
263 acc gag tgg cta caa tcg gta aaa tgg tac tgg aaa caa gaa gac aaa	3071
264 Thr Glu Trp Leu Gln Ser Val Lys Trp Tyr Trp Lys Gln Glu Asp Lys	
265 930 935 940	
267 ata att gaa aat aat acc gct tct aaa aga cat gtg ggt cgt cag gcc	3119
268 Ile Ile Glu Asn Asn Thr Ala Ser Lys Arg His Val Gly Arg Gln Ala	
269 945 950 955	
271 ggc ttt ccc aaa gac tac ttg caa gta aaa caa tcg tat aaa gtt aga	3167
272 Gly Phe Pro Lys Asp Tyr Leu Gln Val Lys Gln Ser Tyr Lys Val Arg	
273 960 965 970 975	
275 ctt gtg ctc tat gga gag agg tat aat gat cta gag aag cat gta tgt	3215
276 Leu Val Leu Tyr Gly Glu Arg Tyr Asn Asp Leu Glu Lys His Val Cys	
277 980 985 990	
279 tca ata aaa cat ggt gac att cat ttt gat cat ttt cac cca tgt gct	3263
280 Ser Ile Lys His Gly Asp Ile His Phe Asp His Phe His Pro Cys Ala	
281 995 1000 1005	
283 gca cta aca aca gat cat att gaa agg tat gga ttc cct cct gat	3308
284 Ala Leu Thr Thr Asp His Ile Glu Arg Tyr Gly Phe Pro Pro Asp	
285 1010 1015 1020	
287 ctt acc ctt tca cct cga gaa agc atc cag ctg tat gat gcc atg	3353
288 Leu Thr Leu Ser Pro Arg Glu Ser Ile Gln Leu Tyr Asp Ala Met	
289 1025 1030 1035	
291 ttt caa att tgg aaa agt tgg cct cgg gcc cag gaa ctg tgc cca	3398
292 Phe Gln Ile Trp Lys Ser Trp Pro Arg Ala Gln Glu Leu Cys Pro	
293 1040 1045 1050	
295 gaa aac ttc att cat ttt aac aat aaa tta gtc att aaa aag atg	3443
296 Glu Asn Phe Ile His Phe Asn Asn Lys Leu Val Ile Lys Lys Met	
297 1055 1060 1065	
299 gat gct agg aaa tat gaa gag agt cta aag gca gaa tta aca agt	3488
300 Asp Ala Arg Lys Tyr Glu Glu Ser Leu Lys Ala Glu Leu Thr Ser	
301 1070 1075 1080	
303 tgg att aaa aat ggc aac gta gag cag gcc aga atg gta ctt cag	3533
304 Trp Ile Lys Asn Gly Asn Val Glu Gln Ala Arg Met Val Leu Gln	
305 1085 1090 1095	
307 aat ctt agt cct gaa gca gat ttg agt cca gaa aac atg atc acc	3578
308 Asn Leu Ser Pro Glu Ala Asp Leu Ser Pro Glu Asn Met Ile Thr	
309 1100 1105 1110	
311 atg ttt cca ctt cta gtt gaa aaa cta agg aaa atg gag aag tta	3623
312 Met Phe Pro Leu Leu Val Glu Lys Leu Arg Lys Met Glu Lys Leu	
313 1115 1120 1125	
314 cct gca cta ttt ttt tta ttc aag tta gga gct gta gaa aac gca	3668
315 Pro Ala Leu Phe Phe Leu Phe Lys Leu Gly Ala Val Glu Asn Ala	
316 1130 1135 1140	
318 gct gaa agt gtg agc act ttc cta aag aaa aag cag gag aca aaa	3713

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:29 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1, Line#:27